

Package ‘armDNA’

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Type Package

Title Age-related DNA methylation

Version 1.0

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Depends nlme, parallel, R (>= 2.14)

Description Detect age-related genomewide DNA methylation marks based on a functional beta model.

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LazyLoad yes

NeedsCompilation no

URL <http://github.com/zhanghfd/armDNA>

BugReports <http://github.com/zhanghfd/armDNA/issues>

RoxygenNote 5.0.1

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armDNA-package	<i>Age-related DNA methylation</i>
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Description

This R package is developed to detect age-related genomewide DNA methylation marks based on a functional beta model using mDNA data obtained through the widely used bisulfite conversion technique. Let mDNA be the beta value defined as $(M+50)/(M+U+100)$, where M and U are methylated profile and unmethylated profile, respectively, then the mean mDNA profile is related to the age and covariates through the following functional beta model:

$$\text{logitE(mDNA)} = \text{beta0} + \text{beta1} * H(\text{Age}) + \text{beta2} * \text{Covar},$$

where $H()$ is an increasing transformation function, and Covar is a covariate vector. The unknown parameters beta0, beta1, beta2 are mDNA-mark dependent. $H()$ is independent of mDNA-marks, which can either be estimated nonparametrically or be specified to be a power function.

$H()$ is assumed to be a piecewise linear function with K nodes (K sample quantiles of ages) if $H()$ is estimated; otherwise, $H()$ is a prespecified power transformation function.

Multiple CPUs can be used to speed up the algorithm through parallel computation.

Details

Package: armDNA
 Type: Package
 Version: 1.0
 Date: 2016-08-03
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Author(s)

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References

Wang C, Shen Q, Du L, Xu J, and Zhang H (2016). armDNA: A functional beta model for detecting age-related genomewide DNA methylation marks

armDNA

Analysis of the effects of age and covariates on mDNA profiles.

Description

This function estimates and tests the effects of age and covariates on mDNA profiles. The transformation function for the age effect on the mDNA profiles can be either estimated nonparametrically or specified to be a power transformation function. Multiple CPUs can be utilized through parallel computation.

Usage

```
armDNA(dat, pow=NULL, age.num=5, cl.cores=1)
```

Arguments

<code>dat</code>	A list contains three variables, namely age (x), mDNA profile (y) and covariate (z), where x is a n -vector (the sample size), y is a $n \times m$ matrix (m : the number of mDNA marks), z is a $n \times p$ matrix (p : the number of covariates).
<code>pow</code>	This can be used to specify the transformation function for the age effect, which should be either NULL (unknown piecewise linear transformation will be estimated) or a positive number (a power transformation will be specified).
<code>age.num</code>	The number of nodes for the age effects, which should be an integer greater than 2, with the default value 5. This parameter should be specified only if "pow" = NULL.
<code>cl.cores</code>	The number of CPU cores used in parallel computation, which should be a positive integer, with the default value 1 (see the help page for the R package "parallel").

Value

<code>par</code>	Estimates of the effects of age and covariates on methylation profile. Column 1 is for the age effects, and columns 2 through $p+1$ are for covariate effects
<code>se</code>	Standard errors of "par"
<code>p.value</code>	P-values for Wald test of the effects of age and covariates on methylation profile
<code>age.h</code>	Estimated transformation function result. If "pow" is a positive number, "age.h" is NULL; if "pow"=NULL, "age.h" is a $\text{age.num} \times 2$ matrix, with the first column being the age values at <code>age.num</code> nodes and the second column being the corresponding estimated H values.

Author(s)

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Examples

```
data(data);
#####
# Not run:
# res = armDNA(data);
```

data

Example data

Description

This is a simulated dataset used to illustrate the performance of armDNA.

Usage

```
data(data)
```

Format

A list containing three variables for 200 samples and 1000 DNA methylation marks.

x A vector for age of 200 samples

y A matrix for DNA methylation profiles of 200 samples at 1000 marks

z A matrix for 1 covariate of 200 samples

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